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RAW SEQUENCE LISTING

DATE: 09/26/2001

PATENT APPLICATION: US/09/942,021

TIME: 13:55:27

Input Set : N:\Crif3\RULE60\09942021.txt

Output Set: N:\CRF3\09262001\I942021.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: Little, Roger G. II
8 (ii) TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability
9 Increasing (BPI) Protein Products
11 (iii) NUMBER OF SEQUENCES: 2
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: McAndrews, Held & Malloy, Ltd.
15 (B) STREET: 500 W. Madison Street, 34th Floor
16 (C) CITY: Chicago
17 (D) STATE: Illinois
18 (E) COUNTRY: USA
19 (F) ZIP: 60661
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/09/942,021
C--> 29 (B) FILING DATE: 27-Aug-2001
30 (C) CLASSIFICATION:
44 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 09/220,427
34 (B) FILING DATE: 24-DEC-1998
37 (A) APPLICATION NUMBER: 08/415,158
38 (B) FILING DATE: March 31, 1995
41 (A) APPLICATION NUMBER: 08/093,202
42 (B) FILING DATE: July 15, 1993
45 (A) APPLICATION NUMBER: 08/030,644
46 (B) FILING DATE: March 12, 1993
C--> 48 (viii) ATTORNEY/AGENT INFORMATION:
49 (A) NAME: McNicholas, Janet M.
50 (B) REGISTRATION NUMBER: 32,918
51 (C) REFERENCE/DOCKET NUMBER: 11004US07 / 100-224.P1.C3
53 (ix) TELECOMMUNICATION INFORMATION:
54 (A) TELEPHONE: 312/707-8889
55 (B) TELEFAX: 312/707-9155
56 (C) TELEX:
59 (2) INFORMATION FOR SEQ ID NO: 1:
61 (i) SEQUENCE CHARACTERISTICS:
62 (A) LENGTH: 1813 base pairs
63 (B) TYPE: nucleic acid
64 (C) STRANDEDNESS: single
65 (D) TOPOLOGY: linear
67 (ii) MOLECULE TYPE: cDNA
69 (ix) FEATURE:

ENTERED

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70      (A) NAME/KEY: CDS
71      (B) LOCATION: 31..1491
73      (ix) FEATURE:
74      (A) NAME/KEY: mat_peptide
75      (B) LOCATION: 124..1491
77      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
79 CAGGCCTTGA GGTTTTGGCA GCTCTGGAGG ATG AGA GAG AAC ATG GCC AGG GGC      54
80                               Met Arg Glu Asn Met Ala Arg Gly
81                               -31 -30                               -25
83 CCT TGC AAC GCG CCG AGA TGG GTG TCC CTG ATG GIG CTC GTC GCC ATA      102
84 Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile
85                               -20                               -15                               -10
87 GGC ACC GCC GTG ACA GCG GCC GTC AAC CCT GGC GTC GTG GTC AGG ATC      150
88 Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile
89                               -5                               1                               5
91 TCC CAG AAG GGC CTG GAC TAC GCC AGC CAG CAG GGG ACG GCC GCT CTG      198
92 Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu
93 10                               15                               20                               25
95 CAG AAG GAG CTG AAG AGG ATC AAG ATT CCT GAC TAC TCA GAC AGC TTT      246
96 Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe
97                               30                               35                               40
99 AAG ATC AAG CAT CTT GGG AAG GGG CAT TAT AGC TTC TAC AGC ATG GAC      294
100 Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp
101                               45                               50                               55
103 ATC CGT GAA TTC CAG CTT CCC AGT TCC CAG ATA AGC ATG GTG CCC AAT      342
104 Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn
105                               60                               65                               70
107 GTG GGC CTT AAG TTC TCC ATC AGC AAC GCC AAT ATC AAG ATC AGC GGC      390
108 Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly
109                               75                               80                               85
111 AAA TGG AAG GCA CAA AAG AGA TTC TTA AAA ATG AGC GGC AAT TTT GAC      438
112 Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp
113 90                               95                               100                               105
115 CTG AGC ATA GAA GGC ATG TCC ATT TCG GCT GAT CTG AAG CTG GGC AGT      486
116 Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser
117                               110                               115                               120
119 AAC CCC ACG TCA GGC AAG CCC ACC ATC ACC TGC TCC AGC TGC AGC AGC      534
120 Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser
121                               125                               130                               135
123 CAC ATC AAC AGT GTC CAC GTG CAC ATC TCA AAG AGC AAA GTC GGG TGG      582
124 His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp
125                               140                               145                               150
127 CTG ATC CAA CTC TTC CAC AAA AAA ATT GAG TCT GCG CTT CGA AAC AAG      630
128 Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys
129                               155                               160                               165
131 ATG AAC AGC CAG GTC TGC GAG AAA GTG ACC AAT TCT GTA TCC TCC AAG      678
132 Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys
133 170                               175                               180                               185
135 CTG CAA CCT TAT TTC CAG ACT CTG CCA GTA ATG ACC AAA ATA GAT TCT      726

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136	Leu	Gln	Pro	Iyr	Phe	Gln	Thr	Leu	Pro	Val	Met	Thr	Lys	Ile	Asp	Ser	
137					190					195					200		
139	GTG	GCT	GGA	ATC	AAC	TAT	GGT	CTG	GTG	GCA	CCT	CCA	GCA	ACC	ACG	GCT	774
140	Val	Ala	Gly	Ile	Asn	Tyr	Gly	Leu	Val	Ala	Pro	Pro	Ala	Thr	Thr	Ala	
141				205					210					215			
143	GAG	ACC	CTG	GAT	GTA	CAG	ATG	AAG	GGG	GAG	TTT	TAC	AGT	GAG	AAC	CAC	822
144	Glu	Thr	Leu	Asp	Val	Gln	Met	Lys	Gly	Glu	Phe	Tyr	Ser	Glu	Asn	His	
145			220					225					230				
147	CAC	AAT	CCA	CCT	CCC	TTT	GCT	CCA	CCA	GTG	ATG	GAG	TTT	CCC	GCT	GCC	870
148	His	Asn	Pro	Pro	Pro	Phe	Ala	Pro	Pro	Val	Met	Glu	Phe	Pro	Ala	Ala	
149		235					240					245					
151	CAT	GAC	CGC	ATG	GTA	TAC	CTG	GGC	CTC	TCA	GAC	TAC	TTC	TTC	AAC	ACA	918
152	His	Asp	Arg	Met	Val	Tyr	Leu	Gly	Leu	Ser	Asp	Tyr	Phe	Phe	Asn	Thr	
153	250					255				260						265	
155	GCC	GGG	CTT	GTA	TAC	CAA	GAG	GCT	GGG	GTC	TTG	AAG	ATG	ACC	CTT	AGA	966
156	Ala	Gly	Leu	Val	Tyr	Gln	Glu	Ala	Gly	Val	Leu	Lys	Met	Thr	Leu	Arg	
157				270						275					280		
159	GAT	GAC	ATG	ATT	CCA	AAG	GAG	TCC	AAA	TTT	CGA	CTG	ACA	ACC	AAG	ITC	1014
160	Asp	Asp	Met	Ile	Pro	Lys	Glu	Ser	Lys	Phe	Arg	Leu	Thr	Thr	Lys	Phe	
161			285						290					295			
163	TTT	GGA	ACC	TTC	CTA	CCT	GAG	GTG	GCC	AAG	AAG	TTT	CCC	AAC	ATG	AAG	1062
164	Phe	Gly	Thr	Phe	Leu	Pro	Glu	Val	Ala	Lys	Lys	Phe	Pro	Asn	Met	Lys	
165		300						305					310				
167	ATA	CAG	ATC	CAT	GTC	ICA	GCC	TCC	ACC	CCG	CCA	CAC	CTG	TCT	GTG	CAG	1110
168	Ile	Gln	Ile	His	Val	Ser	Ala	Ser	Thr	Pro	Pro	His	Leu	Ser	Val	Gln	
169		315					320						325				
171	CCC	ACC	GGC	CTT	ACC	TTC	TAC	CCT	GCC	GTG	GAT	GTC	CAG	GCC	TTT	GCC	1158
172	Pro	Thr	Gly	Leu	Thr	Phe	Tyr	Pro	Ala	Val	Asp	Val	Gln	Ala	Phe	Ala	
173	330					335					340					345	
175	GTC	CTC	CCC	AAC	TCC	CTG	GCT	TCC	CTC	TTT	CTG	ATT	GGC	ATG	CAC		1206
176	Val	Leu	Pro	Asn	Ser	Ser	Leu	Ala	Ser	Leu	Phe	Leu	Ile	Gly	Met	His	
177				350						355					360		
179	ACA	ACT	GGT	TCC	ATG	GAG	GTC	AGC	GCC	GAG	TCC	AAC	AGG	CTT	GTT	GGA	1254
180	Thr	Thr	Gly	Ser	Met	Glu	Val	Ser	Ala	Glu	Ser	Asn	Arg	Leu	Val	Gly	
181			365						370					375			
183	GAG	CTC	AAG	CTG	GAT	AGG	CTG	CTC	CTG	GAA	CTG	AAG	CAC	TCA	AAT	ATT	1302
184	Glu	Leu	Lys	Leu	Asp	Arg	Leu	Leu	Leu	Glu	Leu	Lys	His	Ser	Asn	Ile	
185			380						385					390			
187	GGC	CCC	TTC	CCG	GTT	GAA	TTG	CTG	CAG	GAT	ATC	ATG	AAC	TAC	ATT	GTA	1350
188	Gly	Pro	Phe	Pro	Val	Glu	Leu	Leu	Gln	Asp	Ile	Met	Asn	Tyr	Ile	Val	
189		395					400					405					
191	CCC	ATT	CTT	GTG	CTG	CCC	AGG	GTT	AAC	GAG	AAA	CTA	CAG	AAA	GGC	TTC	1398
192	Pro	Ile	Leu	Val	Leu	Pro	Arg	Val	Asn	Glu	Lys	Leu	Gln	Lys	Gly	Phe	
193	410					415					420					425	
195	CCT	CTC	CCG	ACG	CCG	GCC	AGA	GTC	CAG	CTC	TAC	AAC	GTA	GTG	CTT	CAG	1446
196	Pro	Leu	Pro	Thr	Pro	Ala	Arg	Val	Gln	Leu	Tyr	Asn	Val	Val	Leu	Gln	
197				430						435					440		
199	CCT	CAC	CAG	AAC	TTC	CTG	CTG	TTC	GGT	GCA	GAC	GTT	GTC	TAT	AAA		1491
200	Pro	His	Gln	Asn	Phe	Leu	Leu	Phe	Gly	Ala	Asp	Val	Val	Tyr	Lys		

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201          445          450          455
203 TGAAGGCACC AGGGGTGCCG GGGGCTGTCA GCCGCACCTG TTCCTGATGG GCTGTGGGGC 1551
205 ACCGGGTGCC TTICCCAGG GAACTCTCTC CAGATCTTAA CCAAGAGCCC CITGCAAAC 1611
207 TCTTCGACIC AGATTCAGAA ATGATCTAAA CACGAGGAAA CATTATTCAT TGGAAAAGTG 1671
209 CATGGTGIGI AITTTAGGGA TTATGAGCTT CTTTCAAGGG CTAAGGCTGC AGAGATATTT 1731
211 CCTCCAGGAA TCGTGTTCAT ATTGTAACCA AGAAATTTCC ATTTGTGCTT CATGAAAAAA 1791
213 AACTTCTGGT TTTTTCATG TG 1813
216 (2) INFORMATION FOR SEQ ID NO: 2:
218 (i) SEQUENCE CHARACTERISTICS:
219 (A) LENGTH: 487 amino acids
220 (B) TYPE: amino acid
221 (D) TOPOLOGY: linear
223 (ii) MOLECULE TYPE: protein
225 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
227 Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val
228 -31 -30 -25 -20
230 Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val
231 -15 -10 -5 1
233 Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala
234 5 10 15
236 Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys
237 20 25 30
239 Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
240 35 40 45
242 His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser
243 50 55 60 65
245 Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
246 70 75 80
248 Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
249 85 90 95
251 Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
252 100 105 110
254 Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr
255 115 120 125
257 Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
258 130 135 140 145
260 Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
261 150 155 160
263 Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
264 165 170 175
266 Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu
267 180 185 190
269 Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
270 195 200 205
272 Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
273 210 215 220 225
275 Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
276 230 235 240
278 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly

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279          245          250          255
281 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala
282          260          265          270
284 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
285          275          280          285
287 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
288 290          295          300          305
290 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
291          310          315          320
293 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
294          325          330          335
296 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
297          340          345          350
299 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
300          355          360          365
302 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
303 370          375          380          385
305 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
306          390          395          400
308 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
309          405          410          415
311 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
312          420          425          430
314 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
315          435          440          445
317 Gly Ala Asp Val Val Tyr Lys
318 450          455

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VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:48 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]